R. Schwooren 1644

INPUT SET: S32381.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

#9

SEQUENCE LISTING   ENTERED

```
 1
 2
 3   (1)     General Information:
 4
 5        (i)  APPLICANT:   SCHENDEL, Dolores J.
 6
 7       (ii)  TITLE OF INVENTION:  T CELLS SPECIFIC FOR KIDNEY CARCINOMA
 8
 9      (iii)  NUMBER OF SEQUENCES: 44
10
11       (iv)  CORRESPONDENCE ADDRESS:
12            (A)    ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
13            (B)    STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
14            (C)    CITY: Washington
15            (D)    STATE: DC
16            (E)    COUNTRY: USA
17            (F)    ZIP: 20005-5701
18
19        (v)  COMPUTER READABLE FORM:
20            (A)    MEDIUM TYPE: Floppy disk
21            (B)    COMPUTER: IBM PC compatible
22            (C)    OPERATING SYSTEM: PC-DOS/MS-DOS
23            (D)    SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25       (vi)  CURRENT APPLICATION DATA:
26            (A)    APPLICATION NUMBER: 08/881,509
27            (B)    FILING DATE: June 24, 1997
28            (C)    CLASSIFICATION:
29
30     (viii)  ATTORNEY/AGENT INFORMATION:
31            (A)    NAME: Kitts, Monica Chin
32            (B)    REGISTRATION NUMBER: 36,105
33            (C)    REFERENCE/DOCKET NUMBER: 564-7015
34
35       (ix)  TELECOMMUNICATION INFORMATION:
36            (A)    TELEPHONE: (202) 638-5000
37            (B)    TELEFAX: (202) 638-4810
38
39
40   (2) INFORMATION FOR SEQ ID NO: 1:
41
42   (i) SEQUENCE CHARACTERISTICS:
43            (A) LENGTH: 1341 base pairs
44            (B) TYPE: nucleic acid
45            (C) STRANDEDNESS: both
46            (D) TOPOLOGY: linear
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/881,509A*

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47
48          (ix) FEATURE:
49              (A) NAME/KEY: CDS
50              (B) LOCATION:1..801
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52          (ix) FEATURE:
53              (A) NAME/KEY: sig_peptide
54              (B) LOCATION:1..54
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56          (ix) FEATURE:
57              (A) NAME/KEY: mat_peptide
58              (B) LOCATION:55..801
59
60          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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62      ATG AGG CAA GTG GCG AGA GTG ATC GTG TTC CTG ACC CTG AGT ACT TTG          48
63      Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
64      -18         -15             Val         -10             Ser -5
65
66      AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA          96
67      Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
68              1               5               10
69
70      CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT          144
71      Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
72      15                  20                  25                  30
73
74      TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT          192
75      Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
76                      35                  40                  45
77
78      ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC TCC CTG TTT          240
79      Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
80                  50                  55                  60
81
82      ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC          288
83      Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
84              65                  70                  75
85
86      CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG          336
87      Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
88          80                  85                  90
89
90      CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC          384
91      Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
92      95                  100                 105                 110
93
94      CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT          432
95      Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
96                  115                 120                 125
97
98      GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG          480
99      Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
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102   TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA        528
103   Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
104           145                  150                  155
105
106   GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC        576
107   Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
108           160                  165                  170
109
110   AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT        624
111   Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
112   175                  180                  185                  190
113
114   CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG        672
115   Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
116                  195                  200                  205
117
118   CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC        720
119   Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
120           210                  215                  220
121
122   CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT        768
123   Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
124           225                  230                  235
125
126   AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA      821
127   Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
128           240                  245
129
130   GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG      881
131
132   AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCCGGCA      941
133
134   ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA      1001
135
136   CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA      1061
137
138   GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC      1121
139
140   CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCCTGGAG      1181
141
142   AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTCATA AAGAAATACA TAGTATTCTT      1241
143
144   CTTCTCAAGA CGTGGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG      1301
145
146   GGCGTGTTGT ATGTCCTGCT GCCGATGCCT TCATTAAAAT                             1341
147
148
149   (2) INFORMATION FOR SEQ ID NO: 2:
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151   (i) SEQUENCE CHARACTERISTICS:
152           (A) LENGTH: 267 amino acids
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153                (B) TYPE: amino acid
154                (D) TOPOLOGY: linear
155
156           (ii) MOLECULE TYPE: protein
157
158           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
159
160      Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
161      -18         -15                 -10                 -5
162
163      Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
164              1               5                   10
165
166      Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
167       15                 20                  25                  30
168
169      Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
170                   35                  40                  45
171
172      Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
173              50                  55                  60
174
175      Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
176              65                  70                  75
177
178      Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
179          80                  85                  90
180
181      Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
182       95                 100                 105                 110
183
184      Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
185                  115                 120                 125
186
187      Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
188              130                 135                 140
189
190      Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
191              145                 150                 155
192
193      Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
194          160                 165                 170
195
196      Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
197      175                 180                 185                 190
198
199      Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
200                  195                 200                 205
201
202      Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
203                  210                 215                 220
204
205      Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
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INPUT SET: S32381.raw

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206            225                230               235
207
208  Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
209       240              245
210
211
212  (2) INFORMATION FOR SEQ ID NO: 3:
213
214  (i) SEQUENCE CHARACTERISTICS:
215          (A) LENGTH: 936 base pairs
216          (B) TYPE: nucleic acid
217          (C) STRANDEDNESS: both
218          (D) TOPOLOGY: linear
219
220      (ix) FEATURE:
221          (A) NAME/KEY: CDS
222          (B) LOCATION:1..933
223
224      (ix) FEATURE:
225          (A) NAME/KEY: sig_peptide
226          (B) LOCATION:1..63
227
228      (ix) FEATURE:
229          (A) NAME/KEY: mat_peptide
230          (B) LOCATION:64..933
231
232      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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234  ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA        48
235  Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
236  -21 -20              -15                  -10
237
238  GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA        96
239  Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
240   -5               1           5                  10
241
242  CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC       144
243  Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
244          15              20              25
245
246  TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT       192
247  Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
248          30              35              40
249
250  CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC       240
251  Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
252          45              50              55
253
254  GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG       288
255  Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
256   60              65              70              75
257
258  AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC       336
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INPUT SET: S32381.raw

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NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: _SEE ENCLOSED NOTE_

Applicant Must Provide:

☒ An <u>initial</u> or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An <u>initial</u> or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

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